

125923

From: Kaufman, Claire
Sent: Tuesday, June 29, 2004 1:03 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/063,591

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70
Room:Rem 4E85 Serial #:10/063,591 Date:6/29/04

Please search SEQ ID NO:81 and 82
in commercial databases.

Please put results on disk.

Thanks,
Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Milne & Biosis

=> s human chordin-like

L1 1 HUMAN CHORDIN-LIKE

=> d

L1 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN

AN 2004:302643 BIOSIS

DN PREV200400303074

TI hCHL2, a novel chordin-related gene, displays differential expression and complex alternative splicing in human tissues and during myoblast and osteoblast maturation.

AU Oren, Anat; Toporik, Amir; Biton, Sharon; Almogy, Nechama; Eshel, Dani; Bernstein, Jeanne; Savitsky, Kinneret; Rotman, Galit [Reprint Author]

CS Compugen Ltd, 72 Pinchas Rosen St, IL-69512, Tel Aviv, Israel
galitr@compugen.co.il

SO Gene (Amsterdam), (April 28 2004) Vol. 331, No. April 28, pp. 17-31.
print.

ISSN: 0378-1119 (ISSN print).

DT Article

LA English

ED Entered STN: 30 Jun 2004

Last Updated on STN: 30 Jun 2004

Art Unit: 1646

LOCUS AI739159 601 bp mRNA linear EST 20-DEC-
 1999

DEFINITION wi18h06.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2390651 3'
 similar to SW:CA11_CHICK P02457 PROCOLLAGEN ALPHA 1(I) CHAIN
 PRECURSOR. ;, mRNA sequence.

ACCESSION AI739159
 VERSION AI739159.1 GI:5101140
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 601)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can
 be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 949 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 445.

FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2390651"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"
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 /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Co10 was prepared, and ss circles were made in vitro. Following
 HAP purification, this DNA was used as tracer in a
 subtractive hybridization reaction. The driver was PCR-amplified
 CDNAs from a pool of 5,000 clones made from the same library
 (cloneIDs 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaldo. "

Art Unit: 1646

ORIGIN

Query Match 34.0%; Score 588.2; DB 9; Length 601;
 Best Local Similarity 98.7%; Pred. No. 2.5e-87;
 Matches 593; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1112 CCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCC	1171
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Qy	1172 ACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCA	1231
Db	541 ACGAAGTACCCCTGCCGTACCCCTGAGATAGTGGCTGGGAAGTGTGCAAGATTGCCA	482
Qy	1232 GAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCG	1291
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Qy	1292 GGCGGGTCCTCGTCCACACATCGGTATCCCAAGGCCAGACAACCTGCGTCGCTTGCC	1351
Db	421 GGCGGGTCCTCGTCCACACATCGGTATCCCAAGGCCAGACAACCTGCGTCGCTTGCC	362
Qy	1352 CTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAGATGAG	1411
Db	361 CTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAGATGAG	302
Qy	1412 GAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAACCTTCCA	1471
Db	301 GAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAACCTTCCA	242
Qy	1472 CTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACCTCCG	1531
Db	241 CTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACCTCCG	182
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Db	181 ACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTCCTAGCCCAGACCCCTGGAGCT	122
Qy	1592 GAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG	1651
Db	121 GAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG	62
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Qy	1712 A 1712	
Db	1 A 1	

AW083466/c

LOCUS AW083466 391 bp mRNA linear EST 14-OCT-1999

DEFINITION xc02b12.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583071 3'
similar to contains MER22.t1 MER22 repetitive element ;, mRNA
sequence.

ACCESSION AW083466

VERSION AW083466.1 GI:6038542

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 391)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 368.

FEATURES Location/Qualifiers

source 1..391
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2583071"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co21"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI_CGAP_Co18. Library constructed by Life Technologies."

ORIGIN

Query Match 21.9%; Score 380; DB 9; Length 391;
Best Local Similarity 99.7%; Pred. No. 6.8e-53;
Matches 391; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1010 ATCGTCCTGAAGGAGAACATAAGAAAGCCTGTGTGCATGGCGGGAAAGACGTACTCCAC 1069
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Db 391 ATCGTCCTGAAGGAGAACATAAGAAAGCCTGTGTGCATGGCGGGAAAGACGT-CTCCAC 333

Qy 1070 GGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTGCCCTGCATCCTATGCACC 1129
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 GGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTGCCCTGCATCCTATGCACC 273

Qy 1130 TGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGT 1189
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Db 272 TGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGT 213

Qy 1190 CACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGGACAAAGCAGACCC 1249
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Db 212 CACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAAGCAGACCCT 153
Qy 1250 GGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAGGCACCGGGCCGGTCCTCGTCCAC 1309
|||
Db 152 GGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAGGCACCGGGCCGGTCCTCGTCCAC 93
Qy 1310 ACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGGCCTCG 1369
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Db 92 ACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGGCCTCG 33
Qy 1370 GACTTGGTGGAGATCTACCTCTGGAAGCTGGT 1401
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Db 32 GACTTGGTGGAGATCTACCTCTGGAAGCTGGT 1

Art Unit: 1646

LOCUS AF332891 1047 bp mRNA linear HTC 13-JUL-2001
DEFINITION Homo sapiens FKSG37 (FKSG37) mRNA, complete cds.
ACCESSION AF332891
VERSION AF332891.1 GI:12276190
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1047)
AUTHORS Wang, Y.-G. and Gong, L.
TITLE Cloning of FKSG37, a novel gene located on human chromosome 11q14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Wang, Y.-G.
TITLE Direct Submission
JOURNAL Submitted (01-JAN-2001) Beijing Fengkesheng Function Gene
Technology Ltd., 4 Toutiao Lu Chang Street, Xuanwu District,
Beijing 100050, P.R. China
FEATURES
source Location/Qualifiers
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/map="11q14"
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KVTKT"

ORIGIN

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Matches 830; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

Qy      535 GCCTGTGACGGAGCCACAGCAATGCTGTCCCAGTGTGTGGAACCTCACACTCCCTCTGG 594
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Db      21  GCAGGTTGTGAGGCCACAGCAATGCTGTCCCAGTGTGTGGAACCTCACACTCCCTCTGG 80

Qy      595 ACTCCGGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGAT 654
        ||| ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      81  ACTCCGGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGAT 140

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Art Unit: 1646

Qy	655	CTTCAGTGCCCATGAGCTGTCCCCCTCCGCCTGCCAACCAGTGTGTCCCTCTGCAGCTG	714
Db	141	CTTCAGTGCCCATGAGCTGTCCCCCTCCGCCTGCCAACCAGTGTGTCCCTCTGCAGCTG	200
Qy	715	CACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAAGGCTGCCAGCACC	774
Db	201	CACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAAGGCTGCCAGCACC	260
Qy	775	CCTCCCCTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAA-----GTGAGCA	828
Db	261	CCTCCCCTGCCAGACTCCTGCTGCCAAGCTGGCTCCAGCTGGGCTGCT	320
Qy	829	ATCGGATGAAGAGGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATG	888
Db	321	ATGCTCAGTCAGTGAATTTCATCCTTCCTGCCATTGAGACATCCTCAGGATCCATG	380
Qy	889	TTCCAGTGTGGAGAAAGAGAGGCCCCGGCACCCAGCCCCACTGGCCTCAGCGC	948
Db	381	TTCCAGTGTGGAGAAAGAGAGGCCCCGGCACCCAGCCCCACTGGCCTCAGCGC	440
Qy	949	CCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAA	1008
Db	441	CCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAA	500
Qy	1009	GATCGCCTGAAGGAGAACATAAGAAAGCCTGTGCAATGGCGGGAAAGACGTACTCCCA	1068
Db	501	GATCGCCTGAAGGAGAACATAAGAAAGCCTGTGCAATGGCGGGAAAGACGTACTCCCA	560
Qy	1069	CGGGGAGGTGTGGCACCCGGCTTCCGTGCCTTCGGCCCTTGCATCCTATGCAC	1128
Db	561	CGGGGAGGTGTGGCACCCGGCTTCCGTGCCTTCGGCCCTTGCATCCTATGCAC	620
Qy	1129	CTGTGAGGATGGCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCG	1188
Db	621	CTGTGAGGATGGCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCG	680
Qy	1189	TCACCCCGAGAAAGTGGCTGGAAAGTGTGCAAGATTGCCAGAGGACAAAGCAGACCC	1248
Db	681	TCACCCCGAGAAAGTGGCTGGAAAGTGTGCAAGATTGCCAGAGGACAAAGCAGACCC	740
Qy	1249	TGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGTCTCGTCCA	1308
Db	741	TGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGTCTCGTCCA	800
Qy	1309	CACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGGCCTC	1368
Db	801	CACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGGCCTC	860
Qy	1369	GGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAG	1406
Db	861	GGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAG	898

LOCUS AY163868 1368 bp mRNA linear PRI 15-JUL-2003
 DEFINITION Homo sapiens BNF1 mRNA, complete cds.
 ACCESSION AY163868
 VERSION AY163868.1 GI:32492075
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1368)
 AUTHORS Wu,I. and Moses,M.A.
 TITLE BNF-1, a novel gene encoding a putative extracellular matrix
 protein, is overexpressed in tumor tissues
 JOURNAL Gene 311 (C), 105-110 (2003)
 PUBMED 12853144
 REFERENCE 2 (bases 1 to 1368)
 AUTHORS Wu,I. and Moses,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (15-OCT-2002) Surgical Research, The Children's Hospital,
 320 Longwood Ave., Boston, MA 02115, USA
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ORIGIN

Query Match 79.0%; Score 1368; DB 9; Length 1368;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	344	CCCCTGGACTCCACGCTCGAGCCCCCCCAGACATGTTCTGCCTTTCCATGGGAAGAGA	403
Db	61	CCCCTGGACTCCACGCTCGAGCCCCCCCAGACATGTTCTGCCTTTCCATGGGAAGAGA	120
Qy	404	TACTCCCCCGGCAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCCTG	463
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Qy	464	CGCTGTACCTGCTCAGAGGGGCCATGTGAGTTACCGCCTCCACTGTCCGCCTGTC	523
Db	181	CGCTGTACCTGCTCAGAGGGGCCATGTGAGTTACCGCCTCCACTGTCCGCCTGTC	240
Qy	524	CACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGCCAAGTGTGTGGAACCTCAC	583
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Qy	764	TGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGT	823
Db	481	TGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGT	540
Qy	824	GAGCAATCGGATGAAGAGGACAGTGTGCACTGCCATGGGTGAGACATCCTCAGGAT	883
Db	541	GAGCAATCGGATGAAGAGGACAGTGTGCACTGCCATGGGTGAGACATCCTCAGGAT	600
Qy	884	CCATGTTCCAGTGTGCTGGAGAAAGAGAGGGCCGGCACCCAGCCCCACTGGCCTC	943
Db	601	CCATGTTCCAGTGTGCTGGAGAAAGAGAGGGCCGGCACCCAGCCCCACTGGCCTC	660
Qy	944	AGCGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT	1003
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Db 1141 CAGAGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAACAGCCAGATCTTCACTTGACTCAGAT 1200
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Db 1321 CAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG 1368

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:40:34 ; Search time 4714 Seconds
(without alignments)
10971.849 Million cell updates/sec

Title: US-10-063-591-81

Perfect score: 1732

Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

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5: em_estov:*

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9: gb_est1:*

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11: gb_htc:*

12: gb_est3:*

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14: gb_est5:*

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16: em_estom:*

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21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query			Description
			Match	Length	DB	
	1	788.8	45.5	1047	11	AF332891
	2	735	42.4	1485	11	AK007577
c	3	588.2	34.0	601	9	AI739159
	4	513	29.6	525	13	BX480331
	5	477.8	27.6	481	13	BX091758
	6	429.8	24.8	545	12	BI774183
	7	423	24.4	424	9	AL047873
	8	422.4	24.4	756	12	BI112782
	9	405.8	23.4	768	12	BI113110
	10	389.8	22.5	915	10	BE911015
c	11	380	21.9	391	9	AW083466
	12	379.2	21.9	474	10	BF653749
	13	359	20.7	942	12	BI456773
c	14	343.8	19.8	421	9	AA040433
	15	341.6	19.7	716	10	BF134285
c	16	329	19.0	329	9	AI205645
	17	300.4	17.3	629	12	BI067140
	18	294.6	17.0	352	10	AW482630
c	19	285	16.5	667	13	BQ181634
	20	279.2	16.1	373	10	AW425392
c	21	272.8	15.8	398	9	AA042913
c	22	271	15.6	294	14	CB047807
	23	270.2	15.6	368	10	AW356676
	24	270	15.6	294	14	CB047808
	25	267.4	15.4	750	12	BG175998
c	26	259.4	15.0	348	9	AA037778
	27	259.4	15.0	376	9	AV661482
c	28	254.4	14.7	347	9	AI343625
	29	250.8	14.5	452	10	BE629331
c	30	228	13.2	228	10	BF437134
c	31	226.4	13.1	228	10	BF437637
c	32	225.2	13.0	450	12	BI286468
c	33	222.8	12.9	442	10	BE629653
	34	200.4	11.6	770	10	BF181980
	35	190.6	11.0	248	9	AA040432
	36	181.6	10.5	472	9	AA514464
	37	181.4	10.5	476	10	BF354695
	38	179.4	10.4	426	10	BF354693
	39	177.6	10.3	275	9	AA042926
	40	175.2	10.1	245	9	AA040904
	41	171	9.9	939	13	BU514386
	42	157	9.1	855	10	BE799088
c	43	155.2	9.0	1201	13	BX381985
	44	154.6	8.9	1201	13	BX381986
	45	153.4	8.9	275	10	BB513170

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 15:24:44 ; Search time 800 Seconds
(without alignments)
10444.409 Million cell updates/sec

Title: US-10-063-591-81

Perfect score: 1732

Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	1732	100.0	1732	10	US-09-946-374-141	Sequence 141, App
2	1732	100.0	1732	12	US-10-015-395A-141	Sequence 141, App
3	1732	100.0	1732	13	US-10-206-915-281	Sequence 281, App
4	1732	100.0	1732	13	US-10-199-670-281	Sequence 281, App
5	1732	100.0	1732	13	US-10-201-858-281	Sequence 281, App
6	1732	100.0	1732	13	US-10-205-890-281	Sequence 281, App
7	1732	100.0	1732	13	US-10-208-024-281	Sequence 281, App
8	1732	100.0	1732	13	US-10-201-853-281	Sequence 281, App
9	1732	100.0	1732	13	US-10-063-745-81	Sequence 81, Appl
10	1732	100.0	1732	13	US-10-063-512-81	Sequence 81, Appl
11	1732	100.0	1732	13	US-10-063-513-81	Sequence 81, Appl
12	1732	100.0	1732	13	US-10-063-515-81	Sequence 81, Appl
13	1732	100.0	1732	13	US-10-063-549-81	Sequence 81, Appl
14	1732	100.0	1732	13	US-10-063-569-81	Sequence 81, Appl
15	1732	100.0	1732	13	US-10-063-551-81	Sequence 81, Appl
16	1732	100.0	1732	13	US-10-174-581-281	Sequence 281, App
17	1732	100.0	1732	13	US-10-176-483-281	Sequence 281, App
18	1732	100.0	1732	13	US-10-176-749-281	Sequence 281, App
19	1732	100.0	1732	13	US-10-176-914-281	Sequence 281, App
20	1732	100.0	1732	13	US-10-176-915-281	Sequence 281, App
21	1732	100.0	1732	13	US-10-006-485A-141	Sequence 141, App
22	1732	100.0	1732	13	US-10-013-907A-141	Sequence 141, App
23	1732	100.0	1732	13	US-10-015-499A-141	Sequence 141, App
24	1732	100.0	1732	13	US-10-063-555-81	Sequence 81, Appl
25	1732	100.0	1732	13	US-10-063-563-81	Sequence 81, Appl
26	1732	100.0	1732	13	US-10-063-594-81	Sequence 81, Appl
27	1732	100.0	1732	13	US-10-063-553-81	Sequence 81, Appl
28	1732	100.0	1732	13	US-10-063-554-81	Sequence 81, Appl
29	1732	100.0	1732	13	US-10-176-484-281	Sequence 281, App
30	1732	100.0	1732	13	US-10-180-550-281	Sequence 281, App
31	1732	100.0	1732	13	US-10-183-014-281	Sequence 281, App
32	1732	100.0	1732	13	US-10-187-738-281	Sequence 281, App
33	1732	100.0	1732	13	US-10-187-740-281	Sequence 281, App
34	1732	100.0	1732	13	US-10-187-883-281	Sequence 281, App
35	1732	100.0	1732	13	US-10-194-363-281	Sequence 281, App
36	1732	100.0	1732	13	US-10-194-460-281	Sequence 281, App
37	1732	100.0	1732	13	US-10-194-463-281	Sequence 281, App
38	1732	100.0	1732	13	US-10-194-484-281	Sequence 281, App
39	1732	100.0	1732	13	US-10-195-884-281	Sequence 281, App
40	1732	100.0	1732	13	US-10-195-896-281	Sequence 281, App
41	1732	100.0	1732	13	US-10-196-744-281	Sequence 281, App
42	1732	100.0	1732	13	US-10-196-755-281	Sequence 281, App
43	1732	100.0	1732	13	US-10-196-757-281	Sequence 281, App
44	1732	100.0	1732	13	US-10-197-704-281	Sequence 281, App
45	1732	100.0	1732	13	US-10-197-710-281	Sequence 281, App

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 15:12:54 ; Search time 135 Seconds
(without alignments)
7119.814 Million cell updates/sec

Title: US-10-063-591-81

Perfect score: 1732

Sequence: 1 cccacgcgtccgcgccttc.....aaaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
	1	1501.8	86.7	1570	4	US-09-798-051-4	Sequence 4, Appli
	2	822.4	47.5	1839	4	US-09-798-051-1	Sequence 1, Appli
c	3	196.4	11.3	2315	4	US-09-152-060-48	Sequence 48, Appl
	4	194.2	11.2	3856	4	US-09-620-312D-451	Sequence 451, App
	5	102	5.9	7218	1	US-08-232-463-14	Sequence 14, Appl
	6	88.8	5.1	1732	4	US-09-152-060-30	Sequence 30, Appl
	7	60.2	3.5	507	4	US-09-489-039A-1200	Sequence 1200, Ap
c	8	60.2	3.5	516	4	US-09-489-039A-1064	Sequence 1064, Ap
c	9	60.2	3.5	537	4	US-09-489-039A-1065	Sequence 1065, Ap
c	10	60.2	3.5	549	4	US-09-489-039A-1130	Sequence 1130, Ap
	11	60.2	3.5	558	4	US-09-489-039A-1011	Sequence 1011, Ap

12	60.2	3.5	609	4	US-09-489-039A-1177	Sequence 1177, Ap
13	58	3.3	4897	6	5196516-7	Patent No. 5196516
14	57	3.3	53526	3	US-08-658-136-2	Sequence 2, Appli
15	57	3.3	53577	3	US-08-658-136-1	Sequence 1, Appli
16	55.2	3.2	1166	4	US-09-072-596-323	Sequence 323, App
17	55.2	3.2	1166	4	US-09-072-967-328	Sequence 328, App
c 18	51.4	3.0	554	4	US-09-489-039A-1758	Sequence 1758, Ap
c 19	51.4	3.0	570	4	US-09-489-039A-1676	Sequence 1676, Ap
c 20	49.8	2.9	1559	3	US-09-019-095A-7	Sequence 7, Appli
21	49.6	2.9	44453	4	US-09-146-053-5	Sequence 5, Appli
c 22	48.8	2.8	1926	4	US-09-249-585A-2	Sequence 2, Appli
c 23	48.8	2.8	1926	4	US-09-410-399-3	Sequence 3, Appli
c 24	48.8	2.8	2580	3	US-09-050-863-2	Sequence 2, Appli
c 25	48.8	2.8	2580	4	US-09-359-081-2	Sequence 2, Appli
26	48.8	2.8	5452	2	US-09-130-114-1	Sequence 1, Appli
27	48.8	2.8	8705	4	US-09-647-344A-14	Sequence 14, Appl
c 28	48.8	2.8	9600	3	US-08-910-647-1	Sequence 1, Appli
c 29	48.8	2.8	9600	4	US-09-620-925-1	Sequence 1, Appli
c 30	48.8	2.8	10596	1	US-07-884-811-15	Sequence 15, Appl
c 31	48.8	2.8	10596	1	US-07-885-971-15	Sequence 15, Appl
c 32	48.8	2.8	10596	1	US-08-087-783A-15	Sequence 15, Appl
c 33	48.8	2.8	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 34	48.8	2.8	10596	2	US-08-194-087-15	Sequence 15, Appl
c 35	48.8	2.8	10596	5	PCT-US93-04648-15	Sequence 15, Appl
36	48.8	2.8	16080	4	US-09-724-566A-48	Sequence 48, Appl
37	48	2.8	66804	4	US-09-740-041-3	Sequence 3, Appli
c 38	47.6	2.7	473	4	US-09-621-976-14118	Sequence 14118, A
39	47.6	2.7	703	3	US-09-313-300-6	Sequence 6, Appli
c 40	47.6	2.7	1377	2	US-08-810-572A-1	Sequence 1, Appli
c 41	47.6	2.7	1377	4	US-09-290-333-1	Sequence 1, Appli
c 42	47.6	2.7	1377	4	US-09-782-857A-1	Sequence 1, Appli
c 43	47.6	2.7	1377	4	US-09-879-919-21	Sequence 21, Appl
44	46.4	2.7	505	4	US-09-621-976-15639	Sequence 15639, A
c 45	45.8	2.6	289	3	US-09-007-005-17	Sequence 17, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:32:29 ; Search time 708 Seconds
(without alignments)
10392.485 Million cell updates/sec

Title: US-10-063-591-81

Perfect score: 1732

Sequence: 1 cccacgcgtccgcgccttc.....aaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002s:
7: geneseqn2003as:
8: geneseqn2003bs:
9: geneseqn2003cs:
10: geneseqn2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		

1	1732	100.0	1732	3	AAA37064		Aaa37064 Human PRO
2	1732	100.0	1732	4	AAF54300		Aaf54300 DNA encod
3	1732	100.0	1732	4	AAF92098		Aaf92098 Human PRO
4	1732	100.0	1732	6	ABS74418		Abs74418 Human cDN
5	1732	100.0	1732	7	ABX78668		Abx78668 Human PRO
6	1732	100.0	1732	7	ACA75640		Aca75640 Novel hum
7	1732	100.0	1732	7	ACA71120		Aca71120 Human sec

8	1732	100.0	1732	7	ACC87648	Acc87648 Human sec
9	1732	100.0	1732	7	ACC87034	Acc87034 Human sec
10	1732	100.0	1732	7	ACD04207	Acd04207 Human sec
11	1732	100.0	1732	7	ACA69538	Aca69538 cDNA enco
12	1732	100.0	1732	7	ACA90383	Aca90383 Novel hum
13	1732	100.0	1732	7	ACC89490	Acc89490 Human sec
14	1732	100.0	1732	7	ACA98281	Aca98281 Novel hum
15	1732	100.0	1732	7	ACA93923	Aca93923 Human sec
16	1732	100.0	1732	7	ACD15316	Acd15316 Human sec
17	1732	100.0	1732	7	ACD08903	Acd08903 Human sec
18	1732	100.0	1732	7	ACC96823	Acc96823 Human sec
19	1732	100.0	1732	7	ACF15544	Acf15544 Human sec
20	1732	100.0	1732	7	ACA72911	Aca72911 Human PRO
21	1732	100.0	1732	7	ACD03083	Acd03083 Novel hum
22	1732	100.0	1732	7	ACD01898	Acd01898 Novel hum
23	1732	100.0	1732	7	ACA92090	Aca92090 Novel hum
24	1732	100.0	1732	7	ACA89515	Aca89515 cDNA enco
25	1732	100.0	1732	7	ACA73525	Aca73525 Human sec
26	1732	100.0	1732	7	ACA05840	Aca05840 Human sec
27	1732	100.0	1732	7	ACA66674	Aca66674 cDNA enco
28	1732	100.0	1732	7	ACA91204	Aca91204 Novel hum
29	1732	100.0	1732	7	ACD81581	Acd81581 Human cDN
30	1732	100.0	1732	7	ACF20249	Acf20249 Human sec
31	1732	100.0	1732	7	ACF19635	Acf19635 Human sec
32	1732	100.0	1732	7	ACD21923	Acd21923 Human sec
33	1732	100.0	1732	7	ACF13088	Acf13088 Human sec
34	1732	100.0	1732	7	ACD25191	Acd25191 Human sec
35	1732	100.0	1732	7	ACF00240	Acf00240 Human sec
36	1732	100.0	1732	7	ACA60403	Aca60403 Novel hum
37	1732	100.0	1732	7	ACA72297	Aca72297 Novel hum
38	1732	100.0	1732	7	ACD04821	Acd04821 Novel hum
39	1732	100.0	1732	7	ACD18282	Acd18282 Human sec
40	1732	100.0	1732	7	ACD08289	Acd08289 Human sec
41	1732	100.0	1732	7	ACA88723	Aca88723 Novel hum
42	1732	100.0	1732	7	ACA70165	Aca70165 Human sec
43	1732	100.0	1732	7	ACD12387	Acd12387 Novel hum
44	1732	100.0	1732	7	ACC74302	Acc74302 Human sec
45	1732	100.0	1732	7	ACD15930	Acd15930 Human sec

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:34:39 ; Search time 6945 Seconds
(without alignments)
10809.235 Million cell updates/sec

Title: US-10-063-591-81

Perfect score: 1732

Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

```

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description	
		Match	Length	DB	ID		
1	1732	100.0	1732	6	AX092350	AX092350 Sequence	
2	1732	100.0	1732	6	AX376214	AX376214 Sequence	
3	1732	100.0	1732	6	AX697073	AX697073 Sequence	
4	1732	100.0	1732	9	AY358522	AY358522 Homo sapi	
5	1720	99.3	1720	6	BD276565	BD276565 EXTRACELL	
6	1720	99.3	1720	6	AX048199	AX048199 Sequence	
7	1718	99.2	1738	6	AX363203	AX363203 Sequence	
8	1703.4	98.3	1792	6	AX119273	AX119273 Sequence	
9	1694	97.8	1722	6	AX140200	AX140200 Sequence	
10	1687.6	97.4	1722	6	AX140199	AX140199 Sequence	
11	1661	95.9	1722	6	AX140196	AX140196 Sequence	
12	1501.8	86.7	1570	6	AR409072	AR409072 Sequence	
13	1501.8	86.7	1570	6	AX235836	AX235836 Sequence	
14	1368	79.0	1368	9	AY163868	AY163868 Homo sapi	
15	1354.8	78.2	1356	6	AX119269	AX119269 Sequence	
16	1342.8	77.5	1817	6	AX140202	AX140202 Sequence	
17	1336.8	77.2	1405	6	AX363199	AX363199 Sequence	
18	1336	77.1	1517	6	AX363201	AX363201 Sequence	
19	1320.2	76.2	1890	6	AX140198	AX140198 Sequence	
20	1251.6	72.3	1281	6	AX140195	AX140195 Sequence	
21	1223.8	70.7	1290	6	AX119271	AX119271 Sequence	
22	1134.4	65.5	1515	6	AX140201	AX140201 Sequence	
23	1116.6	64.5	1515	6	AX140197	AX140197 Sequence	
24	942.8	54.4	1622	6	AX140203	AX140203 Sequence	
25	835.2	48.2	1516	10	BC019399	BC019399 Mus muscu	
26	822.8	47.5	1567	6	AX140204	AX140204 Sequence	
27	822.4	47.5	1839	6	AR409071	AR409071 Sequence	
28	822.4	47.5	1839	6	AX235833	AX235833 Sequence	
29	796.6	46.0	1428	10	AF338222	AF338222 Mus muscu	
c	30	678.6	39.2	807	6	AX014311	AX014311 Sequence
c	31	678.6	39.2	807	6	BD222190	BD222190 Human nuc
	32	519	30.0	683	9	HSM800814	AL110168 Homo sapi
	33	424.8	24.5	1202	6	AX140205	AX140205 Sequence
	34	359.4	20.8	422	6	AX014296	AX014296 Sequence

	35	359.4	20.8	422	6	BD222175	BD222175 Human nuc
	36	357	20.6	141937	2	AC011686	AC011686 Homo sapi
c	37	357	20.6	230157	9	AP001324	AP001324 Homo sapi
c	38	343.8	19.8	421	6	AX337465	AX337465 Sequence
	39	244	14.1	211452	2	AP002010	AP002010 Homo sapi
	40	216	12.5	3827	6	AX175123	AX175123 Sequence
	41	211.4	12.2	1864	6	AX175120	AX175120 Sequence
	42	211.4	12.2	3291	10	AF296451	AF296451 Mus muscu
	43	210.2	12.1	1803	10	AF321853	AF321853 Mus muscu
	44	208.6	12.0	3601	10	BC050818	BC050818 Mus muscu
	45	208.2	12.0	2750	10	AF305714	AF305714 Mus muscu

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:43:33 ; Search time 46 Seconds
(without alignments)
3093.450 Million cell updates/sec

Title: US-10-063-591-82

Perfect score: 2545

Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
					%
-----	-----	-----	-----	-----	-----

1	2545	100.0	451	4	Q7Z5J3	Q7z5j3 homo sapien
2	1549	60.9	426	11	Q8VEA6	Q8vea6 mus musculu
3	1542	60.6	406	11	Q925I3	Q925i3 mus musculu
4	1342	52.7	281	4	Q9BZ90	Q9bz90 homo sapien
5	959	37.7	194	4	Q9UG17	Q9ug17 homo sapien
6	793	31.2	448	4	Q7Z6V6	Q7z6v6 homo sapien
7	346.5	13.6	2327	13	Q9IBG7	Q9ibg7 xenopus lae
8	321.5	12.6	413	4	Q8N2W7	Q8n2w7 homo sapien
9	304	11.9	1027	13	Q7T3Q2	Q7t3q2 brachydanio
10	299.5	11.8	1028	11	Q9JLL0	Q9jll0 mus musculu
11	299	11.7	1048	13	Q8AWW5	Q8aww5 gallus gall
12	298	11.7	1036	4	Q9NZV1	Q9nzv1 homo sapien
13	295	11.6	955	4	Q96DN2	Q96dn2 homo sapien
14	292	11.5	673	4	Q86WK8	Q86wk8 homo sapien
15	281.5	11.1	940	13	Q57465	Q57465 gallus gall
16	255.5	10.0	4010	11	Q80T14	Q80t14 mus musculu
17	252	9.9	565	4	Q8TF36	Q8tf36 homo sapien
18	252	9.9	685	4	Q8N8U9	Q8n8u9 homo sapien
19	250	9.8	685	11	Q7TN57	Q7tn57 mus musculu
20	248	9.7	898	5	Q8MQG2	Q8mqg2 caenorhabdi
21	248	9.7	909	5	Q17429	Q17429 caenorhabdi
22	248	9.7	960	5	Q8MM07	Q8mm07 caenorhabdi
23	246.5	9.7	751	5	Q9GYX3	Q9gyx3 drosophila
24	246.5	9.7	751	5	Q9W2H2	Q9w2h2 drosophila
25	246	9.7	984	5	Q964I1	Q964i1 halocynthia
26	242	9.5	685	11	Q8CJ69	Q8cj69 mus musculu
27	237.5	9.3	651	4	Q86UZ4	Q86uz4 homo sapien
28	237.5	9.3	4007	4	Q86XX4	Q86xx4 homo sapien
29	212.5	8.3	608	11	Q80V54	Q80v54 mus, musculu
30	210	8.3	286	11	Q8BS96	Q8bs96 mus musculu
31	190	7.5	1637	6	Q9XSV8	Q9xsv8 bos taurus
32	190	7.5	5146	6	Q8SPM4	Q8spm4 bos taurus
33	184.5	7.2	1354	5	Q9VKA7	Q9vka7 drosophila
34	179.5	7.1	4998	11	Q8CG65	Q8cg65 mus musculu
35	176	6.9	429	5	Q09538	Q09538 caenorhabdi
36	176	6.9	816	11	Q8R417	Q8r417 rattus norv
37	176	6.9	894	11	Q88715	Q88715 mus musculu
38	176	6.9	1350	11	Q80Z20	Q80z20 mus musculu
39	175	6.9	1034	11	Q35888	Q35888 rattus norv
40	174	6.8	2768	5	Q9VC00	Q9vc00 drosophila
41	173.5	6.8	324	11	Q8C8N3	Q8c8n3 mus musculu
42	170	6.7	5374	11	Q99ND0	Q99nd0 mus musculu
43	169	6.6	685	6	Q9TTS5	Q9tts5 bos taurus
44	168.5	6.6	284	5	Q8T1D1	Q8t1d1 dictyosteli
45	167.5	6.6	4123	4	Q75851	Q75851 homo sapien

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:40:23 ; Search time 17 Seconds
(without alignments)
1381.391 Million cell updates/sec

Title: US-10-063-591-82

Perfect score: 2545

Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	Description
1	819	32.2	450	1	NRL1_HUMAN	Q9bu40 homo sapien
2	815	32.0	447	1	NRL1_MOUSE	Q920c1 mus musculu
3	806.5	31.7	456	1	NRL1_CHICK	Q90zd5 gallus gall
4	339.5	13.3	940	1	CHRD_BRARE	O57472 brachydanio
5	322	12.7	941	1	CHRD_XENLA	Q91713 xenopus lae
6	321.5	12.6	955	1	CHRD_HUMAN	Q9h2x0 homo sapien
7	288	11.3	948	1	CHRD_MOUSE	Q9z0e2 mus musculu
8	258.5	10.2	1038	1	SOG_DROME	Q24025 drosophila
9	194.5	7.6	2482	1	VWF_PIG	Q28833 sus scrofa
10	186	7.3	1693	1	SAS_DROME	Q04164 drosophila
11	184	7.2	816	1	NEL2_RAT	Q62918 rattus norv
12	178	7.0	5703	1	MU5B_HUMAN	Q9hc84 homo sapien
13	177	7.0	2813	1	VWF_HUMAN	P04275 homo sapien
14	170	6.7	810	1	NEL1_HUMAN	Q92832 homo sapien
15	169	6.6	5376	1	ZAN_MOUSE	O88799 mus musculu
16	165	6.5	354	1	NOV_MOUSE	Q64299 mus musculu
17	163.5	6.4	1262	1	CA13_CHICK	P12105 gallus gall

18	161	6.3	816	1	NEL2_HUMAN	Q99435 homo sapien
19	161	6.3	2813	1	VWF_CANFA	Q28295 canis famil
20	158.5	6.2	1466	1	CA13_HUMAN	P02461 homo sapien
21	158	6.2	816	1	NEL2_MOUSE	Q61220 mus musculu
22	158	6.2	1453	1	CA11_CHICK	P02457 gallus gall
23	156.5	6.1	176	1	CHRD_RAT	Q63148 rattus norv
24	156.5	6.1	1453	1	CA11_MOUSE	P11087 mus musculu
25	156	6.1	810	1	NEL1_RAT	Q62919 rattus norv
26	154.5	6.1	816	1	NEL_CHICK	Q90827 gallus gall
27	154	6.1	1184	1	FBL2_HUMAN	P98095 homo sapien
28	153.5	6.0	3133	1	HMCT_BOMMO	P98092 bombyx mori
29	152.5	6.0	375	1	CE10_CHICK	P19336 gallus gall
30	152	6.0	351	1	NOV_RAT	Q9qzq5 rattus norv
31	152	6.0	357	1	NOV_HUMAN	P48745 homo sapien
32	150	5.9	1460	1	CA11_CANFA	Q9xsj7 canis famil
33	149	5.9	1170	1	TSP2_BOVIN	Q95116 bos taurus
34	148.5	5.8	1238	1	JAG2_HUMAN	Q9y219 homo sapien
35	146.5	5.8	349	1	CTGF_BOVIN	O18739 bos taurus
36	146.5	5.8	1464	1	CA13_MOUSE	P08121 mus musculu
37	146	5.7	349	1	CTGF_HUMAN	P29279 homo sapien
38	146	5.7	867	1	SSPO_BOVIN	P98167 bos taurus
39	146	5.7	1247	1	JAG2_MOUSE	Q9qye5 mus musculu
40	144	5.7	1464	1	CA11_HUMAN	P02452 homo sapien
41	142.5	5.6	1496	1	CA25_HUMAN	P05997 homo sapien
42	141.5	5.6	699	1	ECM2_HUMAN	O94769 homo sapien
43	141	5.5	250	1	WSP2_RAT	Q9jhc6 rattus norv
44	141	5.5	1172	1	TSP2_HUMAN	P35442 homo sapien
45	140.5	5.5	250	1	WSP2_HUMAN	O76076 homo sapien

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:44:29 ; Search time 20 Seconds
(without alignments)
2169.119 Million cell updates/sec

Title: US-10-063-591-82

Perfect score: 2545

Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	959	37.7	194	2	T14746	hypothetical prote
2	322	12.7	941	1	A55195	chordin precursor
3	258.5	10.2	1038	2	T13177	sog protein - frui
4	248	9.7	884	2	T18649	hypothetical prote
5	187	7.3	1348	2	S27812	probable epidermal
6	187	7.3	1348	2	A43917	probable epidermal
7	177	7.0	2813	1	VWHU	von Willebrand fac
8	176	6.9	429	2	T21113	hypothetical prote
9	175	6.9	1034	2	JC5598	mucin - rat
10	169	6.6	5376	2	T42215	zonadhesin - mouse
11	163.5	6.4	886	2	I50694	collagen alpha 1(I
12	158.5	6.2	1466	1	CGHU7L	collagen alpha 1(I
13	158	6.2	615	2	A05269	collagen alpha 1(I

14	157.5	6.2	206	2	S18250	collagen alpha 1(I
15	156.5	6.1	1453	2	S21626	collagen alpha 1(I
16	156	6.1	810	2	T10756	Nel-homolog protei
17	155	6.1	153	2	A27179	collagen alpha 1(I
18	154	6.1	1184	2	A55184	fibulin-2 precurso
19	153.5	6.0	3133	2	S52093	hemocytin - silkwo
20	152.5	6.0	375	2	A41428	CEF-10 protein pre
21	152.5	6.0	1497	2	I49607	procollagen type V
22	152	6.0	357	2	I38069	gene novH protein
23	148.5	5.8	835	2	JP0076	nel protein - chic
24	148.5	5.8	1487	1	CGHU6C	collagen alpha 1(I
25	148	5.8	488	2	A27353	collagen alpha 1(I
26	146.5	5.8	1464	2	S59856	collagen alpha 1(I
27	146	5.7	349	2	A40551	connective tissue
28	146	5.7	1056	2	A53767	mucin MUC5B, trach
29	145.5	5.7	1042	2	A57534	mucin 5AC (clone L
30	144.5	5.7	1492	2	A40333	collagen alpha 1'(
31	144	5.7	1464	1	CGHU1S	collagen alpha 1(I
32	143	5.6	1486	1	B40333	collagen alpha 1(I
33	142.5	5.6	1496	1	CGHU2V	collagen alpha 2(V
34	141	5.5	1172	1	TSHUP2	thrombospondin 2 p
35	139	5.5	379	2	A35669	gene CYR61 protein
36	138	5.4	2555	2	A40043	notch protein homo
37	137.5	5.4	1746	1	S19694	tenascin precursor
38	137.5	5.4	2318	2	S45306	notch 3 protein -
39	135.5	5.3	197	2	T10081	sperm mitochondria
40	135.5	5.3	4006	2	T09070	probable tenascin
41	134	5.3	1487	2	B41182	collagen alpha 1(I
42	133.5	5.2	1178	1	A39804	thrombospondin pre
43	133	5.2	98	2	I49562	alpha-1 type III c
44	131	5.1	348	2	A40578	beta IG-M2 protein
45	131	5.1	1172	2	A42587	thrombospondin 2 p

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:46:19 ; Search time 49 Seconds
(without alignments)
2602.043 Million cell updates/sec

Title: US-10-063-591-82

Perfect score: 2545

Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description

1	2545	100.0	451	9	US-09-965-528-13	Sequence 13, Appl
2	2545	100.0	451	10	US-09-946-374-142	Sequence 142, App
3	2545	100.0	451	12	US-10-206-915-282	Sequence 282, App
4	2545	100.0	451	12	US-10-199-670-282	Sequence 282, App
5	2545	100.0	451	12	US-10-201-858-282	Sequence 282, App
6	2545	100.0	451	12	US-09-969-984-13	Sequence 13, Appl
7	2545	100.0	451	12	US-10-205-890-282	Sequence 282, App
8	2545	100.0	451	12	US-10-208-024-282	Sequence 282, App
9	2545	100.0	451	12	US-10-201-853-282	Sequence 282, App
10	2545	100.0	451	12	US-10-063-745-82	Sequence 82, Appl
11	2545	100.0	451	12	US-10-063-512-82	Sequence 82, Appl
12	2545	100.0	451	12	US-10-063-513-82	Sequence 82, Appl
13	2545	100.0	451	12	US-10-063-515-82	Sequence 82, Appl
14	2545	100.0	451	12	US-10-063-549-82	Sequence 82, Appl
15	2545	100.0	451	12	US-10-063-569-82	Sequence 82, Appl
16	2545	100.0	451	12	US-10-063-551-82	Sequence 82, Appl
17	2545	100.0	451	12	US-10-174-581-282	Sequence 282, App
18	2545	100.0	451	12	US-10-176-483-282	Sequence 282, App
19	2545	100.0	451	12	US-10-176-749-282	Sequence 282, App
20	2545	100.0	451	12	US-10-176-914-282	Sequence 282, App
21	2545	100.0	451	12	US-10-176-915-282	Sequence 282, App
22	2545	100.0	451	12	US-10-006-485A-142	Sequence 142, App
23	2545	100.0	451	12	US-10-013-907A-142	Sequence 142, App
24	2545	100.0	451	12	US-10-015-499A-142	Sequence 142, App
25	2545	100.0	451	12	US-10-063-555-82	Sequence 82, Appl
26	2545	100.0	451	12	US-10-063-563-82	Sequence 82, Appl
27	2545	100.0	451	12	US-10-063-594-82	Sequence 82, Appl
28	2545	100.0	451	12	US-10-063-553-82	Sequence 82, Appl
29	2545	100.0	451	12	US-10-063-554-82	Sequence 82, Appl
30	2545	100.0	451	12	US-10-176-484-282	Sequence 282, App
31	2545	100.0	451	12	US-10-180-550-282	Sequence 282, App
32	2545	100.0	451	12	US-10-183-014-282	Sequence 282, App
33	2545	100.0	451	12	US-10-187-738-282	Sequence 282, App
34	2545	100.0	451	12	US-10-187-740-282	Sequence 282, App
35	2545	100.0	451	12	US-10-187-883-282	Sequence 282, App
36	2545	100.0	451	12	US-10-194-363-282	Sequence 282, App
37	2545	100.0	451	12	US-10-194-460-282	Sequence 282, App
38	2545	100.0	451	12	US-10-194-463-282	Sequence 282, App
39	2545	100.0	451	12	US-10-194-484-282	Sequence 282, App
40	2545	100.0	451	12	US-10-195-884-282	Sequence 282, App
41	2545	100.0	451	12	US-10-195-896-282	Sequence 282, App
42	2545	100.0	451	12	US-10-196-744-282	Sequence 282, App
43	2545	100.0	451	12	US-10-196-755-282	Sequence 282, App
44	2545	100.0	451	12	US-10-196-757-282	Sequence 282, App
45	2545	100.0	451	12	US-10-197-704-282	Sequence 282, App

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:45:04 ; Search time 22 Seconds
(without alignments)
1058.332 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2136.5	83.9	429	4	US-09-798-051-5	Sequence 5, Appli
2	2032.5	79.9	408	4	US-09-798-051-6	Sequence 6, Appli
3	1543	60.6	426	4	US-09-798-051-2	Sequence 2, Appli
4	1470	57.8	405	4	US-09-798-051-3	Sequence 3, Appli
5	814	32.0	452	4	US-09-798-051-9	Sequence 9, Appli
6	330	13.0	217	4	US-09-152-060-71	Sequence 71, Appli
7	322	12.7	940	2	US-08-938-365-4	Sequence 4, Appli
8	322	12.7	941	1	US-08-343-760A-2	Sequence 2, Appli
9	322	12.7	954	2	US-08-749-169A-3	Sequence 3, Appli
10	322	12.7	954	2	US-09-130-032A-3	Sequence 3, Appli
11	322	12.7	954	4	US-09-866-028-7	Sequence 7, Appli

12	321.5	12.6	955	4	US-09-798-051-8	Sequence 8, Appli
13	288	11.3	283	4	US-09-798-051-7	Sequence 7, Appli
14	272.5	10.7	855	2	US-08-938-365-3	Sequence 3, Appli
15	272	10.7	867	2	US-08-938-365-2	Sequence 2, Appli
16	199.5	7.8	441	3	US-08-985-526-3	Sequence 3, Appli
17	177	7.0	2050	2	US-08-347-594A-2	Sequence 2, Appli
18	177	7.0	2813	4	US-09-381-261A-1	Sequence 1, Appli
19	170	6.7	810	2	US-08-820-170A-34	Sequence 34, Appli
20	170	6.7	810	3	US-09-055-699-34	Sequence 34, Appli
21	170	6.7	810	3	US-09-273-565-34	Sequence 34, Appli
22	170	6.7	810	4	US-09-565-538-34	Sequence 34, Appli
23	170	6.7	810	4	US-09-661-468-34	Sequence 34, Appli
24	170	6.7	810	4	US-09-976-165-34	Sequence 34, Appli
25	166.5	6.5	2813	3	US-08-896-449A-2	Sequence 2, Appli
26	166.5	6.5	2813	3	US-09-132-652-2	Sequence 2, Appli
27	161	6.3	816	2	US-08-820-170A-37	Sequence 37, Appli
28	161	6.3	816	3	US-09-055-699-37	Sequence 37, Appli
29	161	6.3	816	3	US-09-273-565-37	Sequence 37, Appli
30	161	6.3	816	4	US-09-565-538-37	Sequence 37, Appli
31	161	6.3	816	4	US-09-661-468-37	Sequence 37, Appli
32	161	6.3	816	4	US-09-976-165-37	Sequence 37, Appli
33	158.5	6.2	623	3	US-09-029-348-3	Sequence 3, Appli
34	158.5	6.2	626	3	US-09-029-348-2	Sequence 2, Appli
35	155.5	6.1	348	1	US-08-468-847B-14	Sequence 14, Appli
36	152.5	6.0	375	1	US-08-468-847B-13	Sequence 13, Appli
37	152	6.0	357	1	US-08-468-847B-17	Sequence 17, Appli
38	152	6.0	357	4	US-09-253-316-25	Sequence 25, Appli
39	149.5	5.9	1238	3	US-09-214-278-5	Sequence 5, Appli
40	149.5	5.9	1238	4	US-09-855-722-5	Sequence 5, Appli
41	149	5.9	217	4	US-09-602-543-5	Sequence 5, Appli
42	149	5.9	235	4	US-09-602-543-4	Sequence 4, Appli
43	148.5	5.8	1212	3	US-09-214-278-3	Sequence 3, Appli
44	148.5	5.8	1212	4	US-09-855-722-3	Sequence 3, Appli
45	146.5	5.8	1461	4	US-09-585-887-9	Sequence 9, Appli

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OM protein - protein search, using sw model

Run on: June 30, 2004, 20:39:48 ; Search time 59 Seconds
(without alignments)
2159.812 Million cell updates/sec

Title: US-10-063-591-82

Perfect score: 2545

Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	2545	100.0	451	3 AAY99382	Aay99382 Human PRO
2	2545	100.0	451	4 AAB66131	Aab66131 Protein o
3	2545	100.0	451	4 AAU29164	Aau29164 Human PRO
4	2545	100.0	451	4 AAB87566	Aab87566 Human PRO
5	2545	100.0	451	4 AAU02749	Aau02749 Novel Hum
6	2545	100.0	451	4 AAB48069	Aab48069 Human ext
7	2545	100.0	451	5 ABG95891	Abg95891 Human sec
8	2545	100.0	451	5 AAU78174	Aau78174 Human cho
9	2545	100.0	451	6 ABU58540	Abu58540 Human PRO

10	2545	100.0	451	6	ABU88088	Abu88088 Novel hum
11	2545	100.0	451	6	ABU84403	Abu84403 Human sec
12	2545	100.0	451	6	ABR66277	Abr66277 Human sec
13	2545	100.0	451	6	ABR65667	Abr65667 Human sec
14	2545	100.0	451	6	ABU99607	Abu99607 Human sec
15	2545	100.0	451	6	ABU82846	Abu82846 Human PRO
16	2545	100.0	451	6	ABU89967	Abu89967 Novel hum
17	2545	100.0	451	6	ABR68216	Abr68216 Human sec
18	2545	100.0	451	6	ABU96269	Abu96269 Novel hum
19	2545	100.0	451	6	ABU92700	Abu92700 Human sec
20	2545	100.0	451	6	ABO08777	Abo08777 Human sec
21	2545	100.0	451	6	ABO02829	Abo02829 Human sec
22	2545	100.0	451	6	ABR74983	Abr74983 Human sec
23	2545	100.0	451	6	ABR94745	Abr94745 Human sec
24	2545	100.0	451	6	ABU85718	Abu85718 Human PRO
25	2545	100.0	451	6	ABU98878	Abu98878 Novel hum
26	2545	100.0	451	6	ABU98093	Abu98093 Novel hum
27	2545	100.0	451	6	ABU91799	Abu91799 Novel hum
28	2545	100.0	451	6	ABU89492	Abu89492 Human PRO
29	2545	100.0	451	6	ABU86333	Abu86333 Human sec
30	2545	100.0	451	6	ABU67546	Abu67546 Human sec
31	2545	100.0	451	6	ABU80574	Abu80574 Human PRO
32	2545	100.0	451	6	ABU90916	Abu90916 Novel hum
33	2545	100.0	451	6	ABO33975	Abo33975 Human sec
34	2545	100.0	451	6	ABR99492	Abr99492 Human sec
35	2545	100.0	451	6	ABR98882	Abr98882 Human sec
36	2545	100.0	451	6	ABO16405	Abo16405 Human sec
37	2545	100.0	451	6	ABR92305	Abr92305 Human sec
38	2545	100.0	451	6	ABO18946	Abo18946 Human sec
39	2545	100.0	451	6	ABR78367	Abr78367 Human sec
40	2545	100.0	451	6	ABU71992	Abu71992 Novel hum
41	2545	100.0	451	6	ABU85103	Abu85103 Novel hum
42	2545	100.0	451	6	ABO00242	Abo00242 Novel hum
43	2545	100.0	451	6	ABO11574	Abo11574 Human sec
44	2545	100.0	451	6	ABO02219	Abo02219 Human sec
45	2545	100.0	451	6	ABU88793	Abu88793 Novel hum